

FIG. 1A Structural motifs in GRBP2

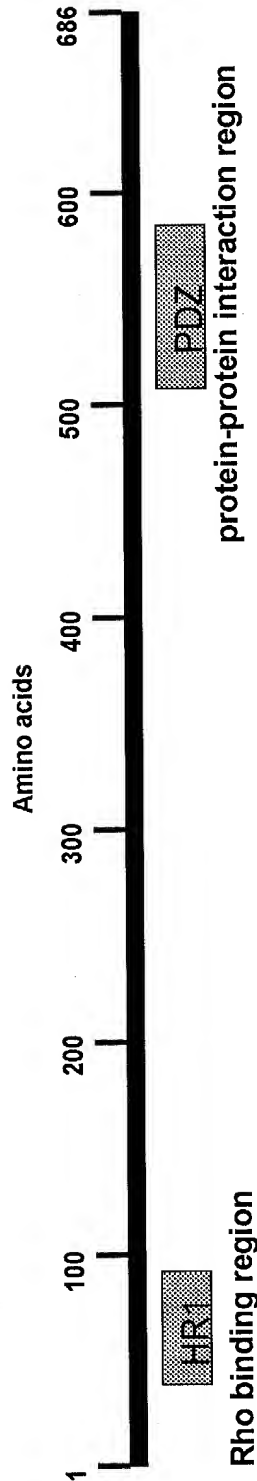


Fig. 1B HR1 domains

		10	20	30	40	50	60
	*.....*.....*.....*.....					
consensus	1	IIILRLPKLIEVLKIREGAEKILRLTSNEKV	11	KKAKSSEAIEKL	21	SNQKIEILL	52
GRBP2	38	nqraalnQQILKAVRMIRGAENLLKVATNSKV	48	REQVRLE	58	VNSDLQML	87
gi 7503594	159	SKLVILQLELEKELKVKRGLEQFLRGAPDKS	169	KVHGDSQSLDD	179	SRAKIAML	209
gi 6093970	42	SHRARLHQQISKELRMTGAENLYRATSNVW	52	RETVALELSYV	62	NSNLQILL	91
gi 543444	216	LRTELRRHHRFVEHVAEAGAKNVRLLSAaKa	226	pDRKAVSEAGKLT	236	SNQKLGIL	270
gi 6319363	5	QLEQNIKKKIATVEENIRGASALKKKTSNVW	15	IQKCNNTIREA	25	RQNLEVL	54
gi 6225859	47	DIKDRIKREIRKELIKEGAENLRKVTIDKK	57	SLAYDNILKK	67	SNKKLEEL	96
gi 1085218	42	VERDRIRKEISRELIKEGAENLRATTERK	52	NLGHVETMLMT	62	CERRLESL	91
gi 1175418	38	KLLEDIKGKLEVECKIRDGAETLLQVDTNFKketkerKEMLKKKCTDeLesSKKKEEL	48		58		97

consensus	53	KQSLR-RLKELH	63
GRBP2	88	KEELE-GINISV	98
gi 7503594	210	RMQIE-RLSQEA	220
gi 6093970	92	KEELA-ELSTSV	102
gi 543444	271	RESLE-RLGELP	282
gi 6319363	55	EDSLK-KIRLKT	65
gi 6225859	97	HHKLQ-EINAH	107
gi 1085218	92	KQELD-GLETPP	102
gi 1175418	98	VSSIE-SFOQEN	108

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Fig. 1C PDZ domains

		10	20	30	40	50	60	
consensus	*.....*.....*.....*						
GRBP2	1	EPRLVELEKGG	---GGLGFLVGGKDSGD	---	GGVVVSVVPSPAAKAG	---	44	
	513	PPRSIRFTAE	---GDLGFTLRGNA	---	PVQHFIDPYCSASVAG	---	551	
gi 13096475	70	PSRLAALRRGTAG	VTGVCLEITYDGSG	---	KDVVLTTPAPGPAEKAG	---	116	
gi 7512038	405	EPRFISFOKE	---GSVGLRLTGGH	---	EAGIFVTAVQPGSPASIQG	---	444	
gi 6671754	484	EPRTVEIIRLS	---DALGISIAGGKSPlg	---	dIPFIAMIQANGVAARTQK	---	531	
gi 7662086	44	VQRCVIIQKQ	---HGFGFTVSGD	---	RVLVQSVRPPGGAAMKAG	---	82	
gi 131530	507	YLVLIIRITPDe	---dGKFGNLLKGGVDq	---	KPFLVVSRIINPEPADTCip	---	551	
gi 6093970	497	LVGPVHMRGE	---GGFGFTLRGD	---	SPVLIAAVVPGQAESAG	---	535	
gi 7499828	46	RPHVVKVVKSE	---TGFGFNKGVSEGGql	rslnqqlYaP	LQHVSAVLRGAADQAG	---	100	
gi 8247939	410	IHVTILHKEEG	---AGLGFSLAGGADlEn	---	KVITVHRVFPNGLASQEGt	---	454	
		70	80	90	100			
	*.....*.....*.....*						
consensus	*.....*.....*						
GRBP2	45	-LKPGEVILEVNG	-TSVEGLTHLEAVDLKE	-AGG	---	KVTLTVLRGG	86	
	552	-AREGDYIVSIQL	-VDCKWLTISEVMKLLKsfGED	---	EEMKVVsl	159		
gi 13096475	117	-ARAGDVITVDG	-TAVKGLSLYDVSLIQG	-EADs	---	QVEWVLHAPG	486	
gi 7512038	445	-LMPGDKILKVN	-MDMNGVTREAVFLLS	-LQD	---	RIDLIVQYCK	573	
gi 6671754	532	-LKVGDRIVS	ING-OPLDGLSHDANLKN	-AFG	---	RIILQVADT	123	
gi 7662086	83	-VKEGDRIIKVNG	tMVTNSS-HLEVVKLIKsg	---	ayVALTLGSS	598		
gi 131530	552	kLNEGQIVLINGr	-DISEHTDQVWF	IKa-SREshsrELa	IVIRRA	578		
gi 6093970	536	-LKEGDYIVSVNG	-QPCKWKHLEVVTLKRS	-MGE	---	GVSILQVWSLL	142	
gi 7499828	101	-LKKGDRILEVNG	-LNVEGSTRKVVDLKN	-GGD	---	ELTMIVISVE	497	
gi 8247939	455	-IQKGNELVLS	ING-KSLKGTTHDALAILRQ	-AREP	---	RQAVIVTRKL		

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For : HUMAN GTP-RHO BINDING
PROTEIN 2

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FIG. 2
Genomic structure of human GRBP2

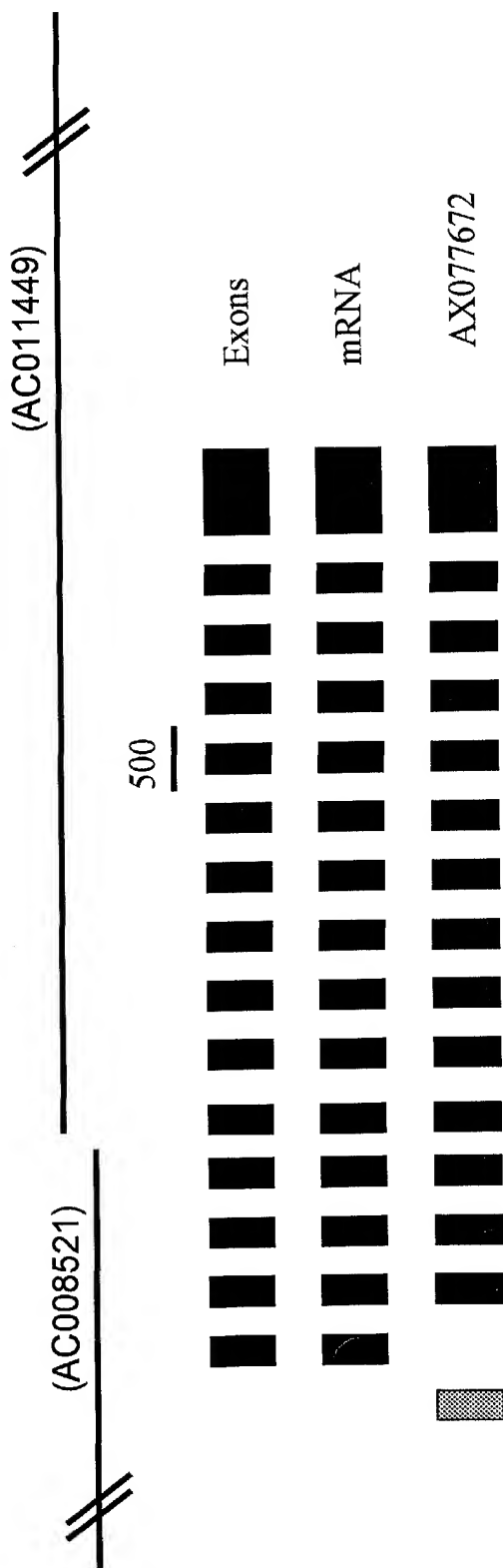


Fig. 3

Nucleotide and protein sequence of the GRBP2 gene

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

								M	T	D	A	L	L	6
tc	cgc	gcc	cgc	gcc	gct	agc	ATG	ACC	GAC	GCG	CTG	TTG		38
P	A	A	P	Q	P	L	E	K	E	N	D	G		19
CCC	GCG	GCC	CCC	CAG	CCG	CTG	GAG	AAG	GAG	AAC	GAC	GGC		77
Y	F	R	K	G	C	N	P	L	A	Q	T	G		32
TAC	TTT	CGG	AAG	GGC	TGT	AAT	CCC	CTT	GCA	CAA	ACC	GGC		116
R	S	K	L	Q	N	Q	R	A	A	L	N	Q		45
CGG	AGT	AAA	TTG	CAG	AAT	CAA	AGA	GCT	GCT	TTG	AAT	CAG		155
Q	I	L	K	A	V	R	M	R	I	G	A	E		58
CAG	ATC	CTG	AAA	GCC	GTG	CGG	ATG	AGG	ATC	GGA	GCG	GAA		194
N	L	L	K	V	A	T	N	S	K	V	R	E		71
AAC	CTT	CTG	AAA	GTG	GCC	ACA	AAC	TCA	AAG	GTG	CGG	GAG		233
Q	V	R	L	E	L	S	F	V	N	S	D	L		84
CAA	GTG	CGG	CTG	GAG	CTG	AGC	TTC	GTC	AAC	TCA	GAC	CTG		272
Q	M	L	K	E	E	L	E	G	L	N	I	S		97
CAG	ATG	CTC	AAG	GAA	GAG	CTG	GAG	GGG	CTG	AAC	ATC	TCG		311
V	G	V	Y	Q	N	T	E	E	A	F	T	I		110
GTG	GGC	GTC	TAT	CAG	AAC	ACA	GAG	GAG	GCA	TTT	ACG	ATT		350
P	L	I	P	L	G	L	K	E	T	K	D	V		124
CCC	CTG	ATT	CCT	CTT	GGC	CTG	AAG	GAA	ACG	AAA	GAC	GTC		389
D	F	A	V	V	L	K	D	F	I	L	E	H		137
GAC	TTT	GCA	GTC	GTC	CTC	AAG	GAT	TTT	ATC	CTG	GAA	CAT		428
Y	S	E	D	G	Y	L	Y	E	D	E	I	A		150
TAC	AGT	GAA	GAT	GGC	TAT	TTA	TAT	GAA	GAT	GAA	ATT	GCA		467
D	L	M	D	L	R	Q	A	C	R	T	P	S		163
GAT	CTT	ATG	GAT	CTG	AGA	CAA	GCT	TGT	CGG	ACG	CCT	AGC		506

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R	D	E	A	G	V	E	L	L	M	T	Y	F	176
CGG	GAT	GAG	GCC	GGG	GTG	GAA	CTG	CTG	ATG	ACA	TAC	TTC	545
I	Q	L	G	F	V	E	S	R	F	F	P	P	189
ATC	CAG	CTG	GGC	TTT	GTC	GAG	AGT	CGA	TTC	TTC	CCG	CCC	584
T	R	Q	M	G	L	L	F	T	W	Y	D	S	201
ACA	CGG	CAG	ATG	GGA	CTC	CTG	TTC	ACC	TGG	TAT	GAC	TCT	623
L	T	G	V	P	V	S	Q	Q	N	L	L	L	214
CTC	ACC	GGG	GTT	CCG	GTC	AGC	CAG	CAG	AAC	CTG	CTG	CTG	662
E	K	A	S	V	L	F	N	T	G	A	L	Y	227
GAG	AAG	GCC	AGT	GTC	CTG	TTC	AAC	ACT	GGG	GCC	CTC	TAC	701
T	Q	I	G	T	R	C	D	R	Q	T	Q	A	240
ACC	CAG	ATT	GGG	ACC	CGG	TGC	GAT	CGG	CAG	ACG	CAG	GCT	740
G	L	E	S	A	I	D	A	F	Q	R	A	A	253
GGG	CTG	GAG	AGT	GCC	ATA	GAT	GCC	TTT	CAG	AGA	GCC	GCA	779
G	V	L	N	Y	L	K	D	T	F	T	H	T	266
GGG	GTT	TTA	AAT	TAC	CTG	AAA	GAC	ACA	TTT	ACC	CAT	ACT	818
P	S	Y	D	M	S	P	A	M	L	S	V	L	279
CCA	AGT	TAC	GAC	ATG	AGC	CCT	GCC	ATG	CTC	AGC	GTG	CTC	857
V	K	M	M	L	A	Q	A	Q	E	S	V	F	292
GTC	AAA	ATG	ATG	CTT	GCA	CAA	GCC	CAA	GAA	AGC	GTG	TTT	896
E	K	I	S	L	P	G	I	R	N	E	F	F	305
GAG	AAA	ATC	AGC	CTT	CCT	GGG	ATC	CGG	AAT	GAA	TTC	TTC	935
M	L	V	K	V	A	Q	E	A	A	K	V	G	318
ATG	CTG	GTG	AAG	GTG	GCT	CAG	GAG	GCT	GCT	AAG	GTG	GGA	974
E	V	Y	Q	Q	L	H	A	A	M	S	Q	A	331
GAG	GTC	TAC	CAA	CAG	CTA	CAC	GCA	GCC	ATG	AGC	CAG	GCG	1013
P	V	K	E	N	I	P	Y	S	W	A	S	L	344
CCG	GTG	AAA	GAG	AAC	ATC	CCC	TAC	TCC	TGG	GCC	AGC	TTA	1052
A	C	V	K	A	H	H	Y	A	A	L	A	H	357
GCC	TGC	GTG	AAG	GCC	CAC	CAC	TAC	GCG	GCC	CTG	GCC	CAC	1091
Y	F	T	A	I	L	L	I	D	H	Q	V	K	370
TAC	TTC	ACT	GCC	ATC	CTC	CTC	ATC	GAC	CAC	CAG	GTG	AAG	1130

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P	G	T	D	L	D	H	Q	E	K	C	L	S	383
CCA	GGC	ACG	GAT	CTG	GAC	CAC	CAG	GAG	AAG	TGC	CTG	TCC	1169
Q	L	Y	D	H	M	P	E	G	L	T	P	L	396
CAG	CTC	TAC	GAC	CAC	ATG	CCA	GAG	GGG	CTG	ACA	CCC	TTG	1208
A	T	L	K	N	D	Q	Q	R	R	Q	L	G	409
GCC	ACA	CTG	AAG	AAT	GAT	CAG	CAG	CGC	CGA	CAG	CTG	GGG	1247
K	S	H	L	R	R	A	M	A	H	H	E	E	422
AAG	TCC	CAC	TTG	CGC	AGA	GCC	ATG	GCT	CAT	CAC	GAG	GAG	1286
S	V	R	E	A	S	L	C	K	K	L	R	S	435
TCG	GTG	CGG	GAG	GCA	AGC	CTC	TGC	AAG	AAG	CTG	CGG	AGC	1325
I	E	V	L	Q	K	V	L	C	A	A	Q	E	448
ATT	GAG	GTG	CTA	CAG	AAG	GTG	CTG	TGT	GCC	GCA	CAG	GAA	1364
R	S	R	L	T	Y	A	Q	H	Q	E	E	D	461
CGC	TCC	CGG	CTC	ACG	TAC	GCC	CAG	CAC	CAG	GAG	GAG	GAT	1403
D	L	L	N	L	I	D	A	P	S	V	V	A	474
GAC	CTG	CTG	AAC	CTG	ATC	GAC	GCC	CCC	AGT	GTT	GTT	GCT	1442
K	T	E	Q	E	V	D	I	I	L	P	Q	F	487
AAA	ACT	GAG	CAA	GAG	GTT	GAC	ATT	ATA	TTG	CCC	CAG	TTC	1481
S	K	L	T	V	T	D	F	F	Q	K	L	G	500
TCC	AAG	CTG	ACA	GTC	ACG	GAC	TTC	TTC	CAG	AAG	CTG	GGC	1520
P	L	S	V	F	S	A	N	K	R	W	T	P	513
CCC	TTA	TCT	GTG	TTT	TCG	GCT	AAC	AAG	CGG	TGG	ACG	CCT	1559
P	R	S	I	R	F	T	A	E	E	G	D	L	526
CCT	CGA	AGC	ATC	CGC	TTC	ACT	GCA	GAA	GAA	GGG	GAC	TTG	1598
G	F	T	L	R	G	N	A	P	V	Q	V	H	539
GGG	TTC	ACC	TTG	AGA	GGG	AAC	GCC	CCC	GTT	CAG	GTT	CAC	1637
F	L	D	P	Y	C	S	A	S	V	A	G	A	552
TTC	CTG	GAT	CCT	TAC	TGC	TCT	GCC	TCG	GTG	GCA	GGA	GCC	1676
R	E	G	D	Y	I	V	S	I	Q	L	V	D	565
CGG	GAA	GGA	GAT	TAT	ATT	GTC	TCC	ATT	CAG	CTT	GTG	GAT	1715
C	K	W	L	T	L	S	E	V	M	K	L	L	578
TGT	AAG	TGG	CTG	ACG	CTG	AGT	GAG	GTT	ATG	AAG	CTG	CTG	1754

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K	S	F	G	E	D	E	I	E	M	K	V	V	591
AAG	AGC	TTT	GGC	GAG	GAC	GAG	ATC	GAG	ATG	AAA	GTC	GTG	1793
S	L	L	D	S	T	S	S	M	H	N	K	S	604
AGC	CTC	CTG	GAC	TCC	ACA	TCA	TCC	ATG	CAT	AAT	AAG	AGT	1832
A	T	Y	S	V	G	M	Q	K	T	Y	S	M	617
GCC	ACA	TAC	TCC	GTG	GGA	ATG	CAG	AAA	ACG	TAC	TCC	ATG	1871
I	C	L	A	I	D	D	D	D	K	T	D	K	630
ATC	TGC	TTA	GCC	ATT	GAT	GAT	GAC	GAC	AAA	ACT	GAT	AAA	1910
T	K	K	I	S	K	K	L	S	F	L	S	W	643
ACC	AAG	AAA	ATC	TCC	AAG	AAG	CTT	TCC	TTC	CTG	AGT	TGG	1949
G	T	N	K	N	R	Q	K	S	A	S	T	L	656
GGC	ACC	AAC	AAG	AAC	AGA	CAG	AAG	TCA	GCC	AGC	ACC	TTG	1988
C	L	P	S	V	G	A	A	R	P	Q	V	K	669
TGC	CTC	CCA	TCG	GTC	GGG	GCT	GCA	CGG	CCT	CAG	GTC	AAG	2027
K	K	L	P	S	P	F	S	L	L	N	S	D	682
AAG	AAG	CTG	CCC	TCC	cct	ttc	agc	ctt	ctc	aac	tca	gac	2066
S	S	W	Y	*									686
agt	tct	tgg	tac	taa	tgt	gag	gaa	aca	aac	atg	ttc	agg	2105
ccc	cga	aca	ttt	ccg	gtg	ctg	act	cgg	cct	taa	acg	ttt	2144
gtg	cca	taa	tgg	aaa	ata	tct	atc	tat	ctg	ttg	tca	aat	2183
cct	gtt	ttt	ctc	ata	gtg	taa	act	cac	att	tga	tgt	gtt	2222
ttt	atg	aag	gaa	agt	aac	caa	gaa	acc	tct	agg	aat	tag	2261
tga	aaa	aag	aac	ttt	ttt	gag	gtg	tgt	tac	tat	act	gct	2300
gta	agt	tat	tta	tta	tat	aaa	gta	ttg	taa	ata	gaa	tag	2339
tgt	tga	aga	tat	gaa	ata	tgg	cta	ctt	tta	atg	gtg	aca	2378
att	atg	act	ttt	agt	cac	tat	taa	att	ggg	gtt	acc	tat	2417
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agg	cag	gtc	aga	gga	ctg	taa	tga	tag	aat	taa	att	agt	2534
gtc	act	aaa	aac	tgt	ccc	aaa	gtg	ctg	ctt	cct	aat	agg	2573

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